## Table S14: Summary of sigma factor-dependency of novel RNA features



(a,b) Summary of sigma factor dependency for short and long features are provided separately. (c) Summary of sigma factor dependency for anti-sense features. (d) Structural relationship of features with Genbank annotations. GB refers to features annotated in Genbank, the new features identified in this work are indicated as in SOM 2. (e) Total number of features per category. (f) Number of features transcribed in a TU associated with a promoter SigA-dependent. (g) Number of features transcribed in a TU associated with a promoter dependent on alternative sigma factors (other than SigA). (h) Number of features transcribed in a TU associated with a promoter dependent of a sporulation sigma factor (SigE, F, G, and K). (i) Number of features transcribed in a TU associated with a promoter dependent of an alternative sigma factor not linked to sporulation (SigB, D, H, I, L, M, W, X, and Y). (j) Number of features for which the prediction of sigma factor dependency is not available (the motif clustering algorithm did not predict a sigma factor binding site with sufficient probability (posterior probability Pcomp > 0.5, Table S4) or the feature is not located in a mapped TU).